

BLASTP 2.2.20+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: YSX4N1PM01R

Database: PDB protein database
40,857 sequences; 9,338,155 total letters

Query=
Length=16

No significant similarity found. For reasons why, [click here](#).

Database: PDB protein database
Posted date: Apr 17, 2009 6:11 PM
Number of letters in database: 2,147
Number of sequences in database: 28

Lambda K H
0.335 0.297 1.50

Gapped

Lambda K H
0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 28

Number of Hits to DB: 172

Number of extensions: 4

Number of successful extensions: 4

Number of sequences better than 200000: 4

Number of HSP's better than 200000 without gapping: 0

Number of HSP's gapped: 4

Number of HSP's successfully gapped: 4

Length of query: 16

Length of database: 2147

Length adjustment: 6

Effective length of query: 10

Effective length of database: 1979

Effective search space: 19790

Effective search space used: 19790

T: 11

A: 40

X1: 1 (0.5 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 1 (3.6 bits)

S2: 0 (3.2 bits)